

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions,
and listings of claims in the application:

LISTING OF CLAIMS:

1-43. (canceled)

44. (withdrawn) Mutated V1/AR1/AV1 or C1/AL1/AC1 gene sequence of a tomato infecting geminivirus wherein the mutations consist of point mutations distributed along the sequence in such a way that the continuous homology between the mutated sequence and the corresponding viral gene sequence is below or equal to 8 nucleotides, preferably below or equal to 5 nucleotides, said mutated sequence encoding for a capsid protein or for a Rep protein, respectively.

45. (withdrawn) Mutated V1/AR1/AV1 gene sequence according to claim 44, encoding for a capsid protein having sequence SEQ ID No 7.

46. (withdrawn) Mutated C1/AL1/AC1 gene sequence according to claim 44, wherein the mutation further comprises a truncation occurring at 3' terminal so that the mutated sequence encodes for a truncated Rep protein.

47. (withdrawn) Mutated C1/AL1 /AC1 gene sequences according to claim 46, wherein the truncated Rep proteins consist of 130 aminoacids (Rep 130) to 210 aminoacids (Rep 210).

48. (withdrawn) Mutated C1/AL1/AC1 gene sequence according to claim 46 encoding for Rep 210 SEQ ID No 3 or SEQ ID No 5.

49. (withdrawn) Mutated C1/AL1/AC1 gene sequence encoding for Rep 130 SEQ ID No 9.

50. (withdrawn) Mutated gene sequence according to claim 44 wherein the tomato infecting geminivirus is TYLCSV.

51. (withdrawn) Synthetic construct comprising an heterologous polynucleotide sequence containing in the 5'-3' direction:

- a) polynucleotide sequence acting as promoter in said plant or tissue or transformed cells;
- b) a non translated polynucleotide sequence positioned 5' of the encoding region;
- c) a mutated gene sequence;
- d) a sequence acting as transcription terminator, positioned 3' with respect to the mutated gene sequence.

52. **(withdrawn)** Expression vector comprising the construct as defined according to claim 51.

53. **(withdrawn)** Transgenic plant, tissue or plant cells thereof, comprising in their genome a mutated gene sequence according to claim 44.

54. **(withdrawn)** Seed comprising in its genome a mutated gene sequence according to claim 44.

55. **(currently amended)** A method for the preparation of transgenic plants, plant tissue or cells thereof having long lasting resistance against geminiviruses, including the following steps:

a) selection of a geminivirus gene-derived C1/AL1/AC1 polynucleotide sequence encoding an amino acid sequence capable of conferring resistance against geminiviruses, said resistance being overcome over time by geminivirus induced post-transcriptional transgene silencing;

b) mutagenesis of the selected geminivirus gene-derived C1/AL1/AC1 polynucleotide sequence, wherein the mutations consist of silent point mutations distributed along the geminivirus gene-derived C1/AL1/AC1 polynucleotide sequence so that continuous homology between the mutated C1/AL1/AC1 polynucleotide sequence and the corresponding viral gene selected C1/AL1/AC1

polynucleotide sequence is less than or equal to 8 nucleotides;
and

c) insertion of the geminivirus gene-derived C1/AL1/AC1
polynucleotide sequence mutated in the step b) in the plant,
plant tissue or cell thereof, using a construct comprising an
heterologous polynucleotide sequence containing in the 5'-3'
direction:

i) a polynucleotide sequence acting as a promoter in said
plant, plant tissue or cells;

ii) a non-translated polynucleotide sequence positioned 5'
of the encoding region of the mutated geminivirus gene-derived
C1/AL1/AC1 polynucleotide sequence;

iii) a mutated C1/AL1/AC1 polynucleotide sequence
mutagenised according to step (b) encoding a mutagenised
geminivirus derived amino acid sequence, mutagenised according to
step (b) and capable to be wherein the mutated C1/AL1/AC1
polynucleotide sequence is an ineffective target of the
geminivirus induced post-transcriptional transgene silencing; and

iv) a polynucleotide sequence acting as a transcription
terminator positioned 3' with respect to said mutated C1/AL1/AC1
polynucleotide sequence encoding a mutagenised geminivirus
derived amino acid sequence.

58. **(previously presented)** The method according to claim 55, wherein the geminiviruses are selected from the species belonging to the Begomovirus genus and isolates thereof.

59. **(previously presented)** The method according to claim 58, wherein the Begomoviruses species is Tomato yellow leaf curl Sardinia virus (TYLCSV).

60-62. **(cancelled)**

63. **(currently amended)** The method according to claim 61 59, wherein the selected geminivirus-derived C1/AL1/AC1 polynucleotide sequence amino acid sequence is encodes a truncated protein with respect to the geminivirus wild-type protein.

64. **(currently amended)** The method according to claim 63 wherein the mutated geminivirus gene derived C1/AL1/AC1 polynucleotide sequence made an ineffective target of the geminivirus-induced post-transcriptional transgene silencing is SEQ ID NO 4 SEQ ID NO: 4.

65. **(currently amended)** The method according to claim 64, wherein the truncated protein is Rep-210 having the sequence of SEQ ID NO 5 SEQ ID NO: 5.

66-67. (cancelled)

68. (previously presented) The method according to claim 55, wherein the plants, plant tissues or cells thereof belong to a member selected from the group consisting of tomato, pepper, tobacco, squash, manioc, sweet potato, cotton, melon, potato, soybean, corn, wheat, sugar cane, bean, and beet.

69. (currently amended) The method according to claim 55, wherein the continuous homology between the mutated C1/AL1/AC1 polynucleotide sequence and the selected C1/AL1/AC1 polynucleotide sequence is less than or equal to 5 nucleotides.